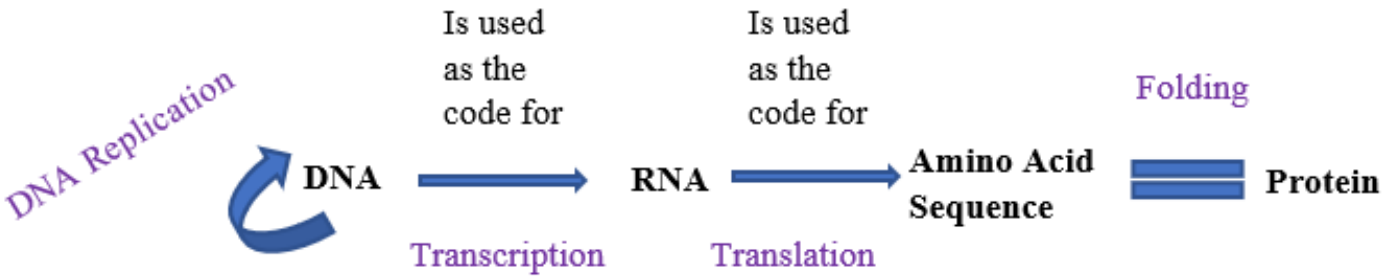
Central Dogma of Biology

Introduction:

The central dogma of biology explains the relationship between DNA, RNA, and proteins. DNA is a genetic code stored in the nucleus of a eukaryotic cell. With this code, an mRNA transcript can be made (transcription). This mRNA transcript can leave the nucleus to interact with a ribosome where it can act as the code for making a protein (translation).

Prokaryotic cells have the same steps, transcription and translation, yet they can do both processes simultaneously. Prokaryotes lack a nucleus, so an mRNA transcript can be transcribed and then immediately used for translation in the same location. Only in prokaryotes can transcription and translation occur simultaneously.



Complete this worksheet one section at a time. Each process is broken down with a table to organize key information first. The section labeled application ties together each of the three processes and provides practice and thought questions about the central dogma of biology.

DNA Replication:

DNA replication is the process of making a new daughter strand of DNA from a pre-existing strand of DNA.

Which of the following is used to guide DNA replication, a template strand or a coding strand? Template

Fill out the table below noting the order each protein is used and the function the protein does during replication. It may be useful to write out the process first then fill in the table.

Protein	Function	Order
DNA polymerase I	Removes RNA primer and replaces it with DNA Proofreads the daughter strand of DNA looking for errors in pairing between the daughter and the template strand. Fills in gaps between Okazaki fragments	6
DNA polymerase III	Makes new strand of DNA by recruiting bases that are complementary to the template strand.	4
Single strand binding proteins (SSBP)	Keeps the DNA from reassociating and closing up so the bases can be accessed.	2
Helicase	Breaks the hydrogen bonds and open up the DNA so it can be accessed and used to guide DNA replication.	1
Primase	Lays a primer (made of RNA) that DNA pol III can sit on.	3
DNA Topoisomerase	Make tiny cuts to unwind the tension in the DNA (Relieves supercoiling)	5 *Note: as soon as the strand begins to have supercoiling, this protein must function. This starts sometime after the DNA is opened up enough to start laying new DNA and will continue until DNA replication ends.
DNA ligase	Glue the pieces together (such as the Okazaki fragments)	7

Transcription:

Transcription is the process of making an mRNA transcript using a strand of DNA.

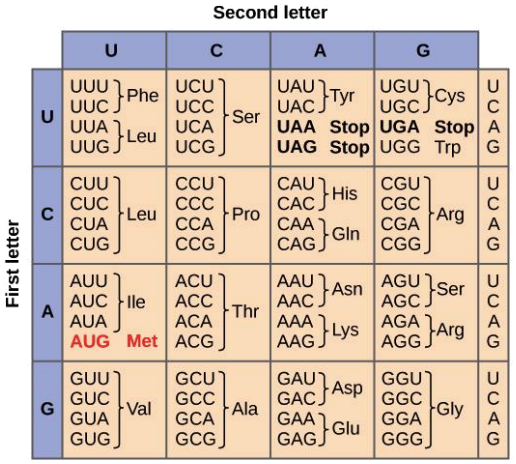
Which of the following is used to guide transcription, a template strand or a coding strand? Template

Explain the process of transcription for prokaryotes and eukaryotes. Underline all of the proteins that make this process possible. Then, take note of which steps and proteins are different between prokaryotes and eukaryotes.

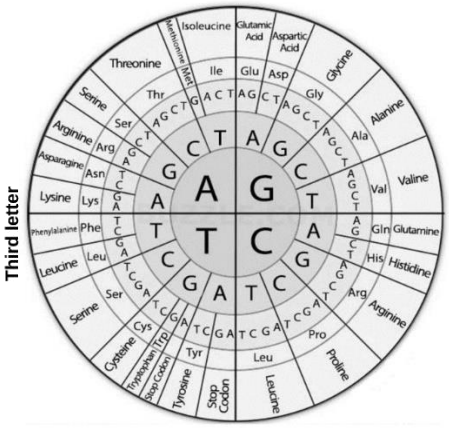
	Eukaryotes	Prokaryotes
Initiation	1. TATA Binding Protein (TBP) binds to the TATA sequence (aka TATA box) in the promoter. 2. General transcription factors and RNA polymerase II assemble. 3. Transcription bubble opens. 4. The C-terminus domain of RNA polymerase II is phosphorylated. 5. Phosphorylation activates the RNA polymerase II resulting in a conformational change and it is freed from the transcription factors.	1. RNA polymerase binds to a promoter 2. Sigma factor (a type of transcription factor specifically for prokaryotes) binds to a specific place in the promoter. 3. RNA polymerase components can assemble at this site; a complex can form. 4. The sigma factor leaves once the complex is formed. 5. The transcription bubble opens.
Elongation	RNA polymerase II "reads" the DNA template strand in the 3' to 5' direction and synthesizes an RNA transcript in the 5' to 3' direction. This protein is moving in one direction due to the antiparallel nature of strands.	Same as elongation for eukaryotes, but co-transcriptional modifications can also occur.
Termination	1. A specific sequence in the DNA template strand is recognized. This sequence is not at the end of the chromosome. 2. RNA is cut downstream of this specific sequence and can dissociate (float away). 3. RNA polymerase II continues reading the DNA template strand until it reaches the terminator sequence. 4. RNA polymerase II dissociates and the replication bubble closes.	Rho independent and rho dependent termination both can occur for transcription in prokaryotes **Rho independent: Hairpin loop method:** 1. An attraction occurs between complementary bases at the end of the RNA transcript. 2. A loop structure is formed. A "G-C" rich region forms the stem portion of the stem-loop structure. 3. Once the loop is formed, the transcript and the complex leaves. **Rho dependent:** 1. Rho protein recognizes a sequence in the mRNA transcript 2. Rho binds 3. Complex and mRNA are released.

Translation:

Translation is the process of using an mRNA transcript to make a protein. A codon (a set of three bases) in the mature mRNA transcript code for a specific amino acid sequence. The amino acid code is redundant; multiple codons code for the same amino acid. Below are two images of codon charts.



First letter	Second letter: U	Second letter: C	Second letter: A	Second letter: G	Third letter
U	UUU, UUC: Phe UUA, UUG: Leu	UCU, UCC, UCA, UCG: Ser	UAU, UAC: Tyr **UAA Stop** **UAG Stop**	UGU, UGC: Cys **UGA Stop** UGG Trp	U C A G
C	CUU, CUC, CUA, CUG: Leu	CCU, CCC, CCA, CCG: Pro	CAU, CAC: His CAA, CAG: Gln	CGU, CGC, CGA, CGG: Arg	U C A G
A	AUU, AUC, AUA: Ile **AUG Met**	ACU, ACC, ACA, ACG: Thr	AAU, AAC: Asn AAA, AAG: Lys	AGU, AGC: Ser AGA, AGG: Arg	U C A G
G	GUU, GUC, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U C A G



Explain the process of translation for prokaryotes and eukaryotes. Underline all of the proteins that make this process possible. Then, note which steps and proteins are different between prokaryotes and eukaryotes. *Note*: Make sure to include the size of each ribosomal subunit and list each step in order.

Initiation	Prokaryotes	1. With the help of initiation factors, small ribosomal subunit (30S) recognizes the Shine Dalgarno sequence and places the start codon (AUG) in the P site. 2. Initiator tRNA carrying a methionine enters the P site. 3. Large ribosomal subunit (50S) binds.
	Eukaryotes	1. With the help of initiation factors, the small ribosomal subunit (40S) with an initiator tRNA in the P site recognizes the 5' guanine cap. 2. The small ribosomal subunit scans the mRNA transcript, one nucleotide at a time, until it recognizes the start codon. 3. The start codon is placed in the P site. 4. The large ribosomal subunit (60S) is called over and binds.
Elongation	1. Charged tRNAs carrying amino acids enter the A site. If they have the complementary anticodon to the codon in the A site, the elongation factor allows them to stay. If they do not, they leave and another is allowed to enter to check compatibility. 2. The ribosome cleaves the amino acid from the tRNA in the P site and attaches it to the growing polypeptide in the A site. 3. The newly uncharged (empty) tRNA moves to the E site to exit and the growing polypeptide (and its tRNA) moves to the P site. A new tRNA checks if it is complementary to the newly centered codon in the A site. 4. This process continues with charged tRNA entering A site, moving to P site with a growing peptide, and exiting in the E site until a stop codon enters the A site.	
Termination	1. A release factor enters the A site and interacts with the stop codon. 2. The release factor promotes the release of the polypeptide. 3. The ribosomal subunits and mRNA transcript are released.	

Application:

Complete the chart:

DNA, RNA, or amino acid sequence?	If DNA: Template or coding?	If RNA: mRNA or tRNA?	Directionality	Sequence	Directionality
DNA	Coding Strand	N.A.	3’	ATTACATGGCCGTTATT	5’
DNA	Template Strand	N.A.	5’	TAATGTACCGGCAATAA	3’
RNA	N.A.	mRNA	3’	AUUACAUGGCCGUUAUU	5’
RNA	N.A.	tRNA	5’	UAAUGUACCGGCAAUAA	3’
Amino acid sequence	N.A.	N.A.	N- Terminus	Met-Tyr-Arg-Gln	C- Terminus

Does this table illustrate the central dogma using a prokaryote or a eukaryote? How do you know?

Prokaryote

Splicing, capping, and tailing were not illustrated in this table. In prokaryotes, mRNA can be used for translation while it is being made and does not require any post-transcriptional modifications. Pre-mRNA is the RNA made directly after transcription in eukaryotes. This cannot be used for translation, only mature mRNA can be used.

How does a pre-mRNA transcript differ from a mature mRNA transcript?

A mature mRNA will have already underwent splicing (removal of introns), any alternative splicing that must occur, and a guanine cap and poly-a tail will have been added.

If alternative splicing was to occur, how would it change what is written in the table above?

Alternative splicing removes all introns as well as some exons resulting in a shorter RNA than one which only underwent splicing and much shorter than the pre-mRNA shown above. Using the new mRNA from alternative splicing would result in a different protein with less amino acids.